



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

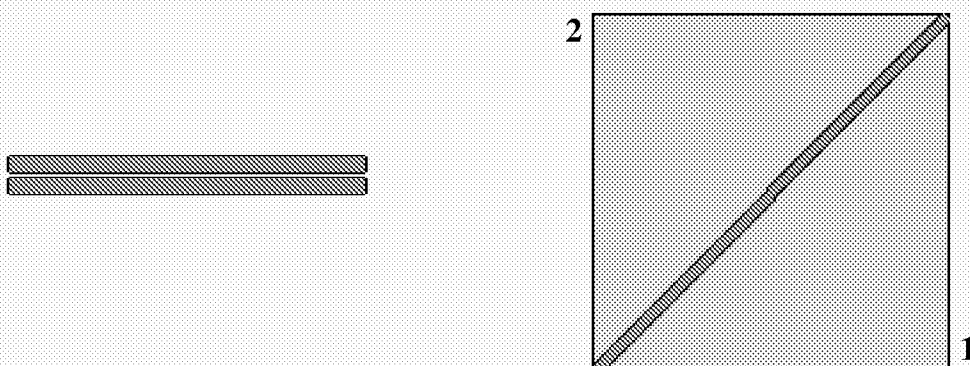
Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix:  gap open:  gap extension:   
x\_dropoff:  expect:  wordsize:  Filter ☒ View option:   
Masking character option:  Masking color option:   
☐ Show CDS translation

**Sequence 1:** gi|6706916|spike glycoprotein [bovine coronavirus] Genbank Accession# AAF25499  
Length = 1363 (1 .. 1363)

**Sequence 2:** unnamed protein product SEQ ID NO: 4  
Length = 1363 (1 .. 1363)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 2625 bits (6803), Expect = 0.0

Identities = 1311/1363 (96%), Positives = 1337/1363 (98%), Gaps = 0/1363 (0%)

Query	1	MFLILLISLPMALAVIGDLKCTTVSINDVDTGVPVSSTDVTDVTNGLGTTYVLDRVYLN	60
		MFLILLISLPMALAVIGDLKCTTVSINDVDTG PS+STD VDTVNTGLGTTYVLDRVYLN	
Sbjct	1	MFLILLISLPMALAVIGDLKCTTVSINDVDTGAPSISTDVVDVTNGLGTTYVLDRVYLN	60
Query	61	TLLNGYYPTSGSTYRNMALKGTLLLSTLWFKPPFLSDFINGIFAKVKNTKVIKNGVMYS	120
		TLLNGYYPTSGSTYRNMALKGTLLLSTLWFKPPFLSDFI+G+FAKVKNTKVIK+GV+YS	
Sbjct	61	TLLNGYYPTSGSTYRNMALKGTLLLSTLWFKPPFLSDFIDGVFAKVKNTKVIKDGVVYS	120
Query	121	EFPAITIGSTFVNTSYSVVVQPHTTNLDNKLQGLLEISVCQYTMCEYPHTICHPNLGNRR	180

Sbjct	121	EFPAITIGSTFVNTSYSVVVQPHHTNLDNKLQGLLEISVCQYTMCDYPHTMCHPNLGNKR	180
Query	181	IELWHWDTGTVVSCLYKRNFYTDVNADYLYHFHYQEGGTFYAYFTDTGVVTKFLFNVYLGT	240
Sbjct	181	IELWHWDTGTVVCLYKRNFYTDVNADYLYSHFYQEGGTFYAYFTDTGVVTKFLFHVYLGT	240
Query	241	VLSHYYVMPLTCNSAMTLEYWVTPLTSKQYLLAFNQDGVIFNAVDCKSDFMSEIKCKTLS	300
Sbjct	241	VLSHYYVMPLTCNSAMTLEYWVTPLT KQYLLAFNQDGVIFNAVDCKSDFMSEIKCKTLS	300
Query	301	IAPSTGVYELNGYTVQPIADVRRIPNLPDCNIEAWLNDKSVPSPLNWERKTFSNCFNM	360
Sbjct	301	IAPSTGVYELNGYTVQPIADVRRIPNLPDCNIEAWLNDKSVPSPLNWERKTFSNCFNM	360
Query	361	SSLMSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPNGRKVDLQGLNGLGYLQSFNYRI	420
Sbjct	361	SSLMSFIQADSFTCNNIDAAKIYGMCF SITIDKFAIPNGRKVDLQ+GNLGLGYLQSFNYRI	420
Query	421	DTTATSCQLYYNLPAANVSVSFRNPNSTWNRFGFTEQSVFKPQPVGVFTDHDVVYAQHCF	480
Sbjct	421	DTTATSCQLYYNLPA+NVS+SRFNPS WNRFGFTEQSVFKPQPVGVFTDHDVVYAQHCF	480
Query	481	KAPT NFCPCKLDGSLCVGSGSIDAGYKNSGIGTCPAGTNYLTCHNAAQCNCCLCTPDPI	540
Sbjct	481	KAPT NFCPCKL+GSLCVGSG GIDAGYKNSGIGTCPAGTNYLTC+NA QC+CLCTPDPI	540
Query	541	SKSTGPYKCPQTKYLVGIGEHCSGLAIKSDYCGGNPCTCQPQAFLGWSVDSCLQGDRNCI	600
Sbjct	541	SKSTGPYKCPQTKYLVGIGEHCSGLAIKSDYCGGNPCTCQP+AFLGWSVDSCLQGDRNCI	600
Query	601	FANFILHDVNSGTTTSTD LQKSNTDIILGVCVNYDLYGITGQGIFVEVNATYYNSWQNLL	660
Sbjct	601	FANFILH VNSGTTTSTD LQKSNTDIILGVCVNYDLYGITGQGIFVEVNATYYNSWQNLL	660
Query	661	YDSNGNLYGFRDYLTNRFTMIRSCYSGRVSAAFHANSSEPALLFRNIKCNYVFNNTLSRQ	720
Sbjct	661	YDSNGNLYGFRDYLTNRFTMIRSCYSGRVSA FH+NSSEPALLFRNIKCNYVFNNTLSRQ	720
Query	721	LQPINYFDSYLGCVVNADNSTSSAVQTCDLTVGSGYCVDYSTKRRSRAITTGyrFTNFE	780
Sbjct	721	LQPINYFDSYLGCVVNADNSTSSSVQTCDLTVGSGYWDYSTQRRSRRTITTGYRFTNFE	780
Query	781	PFTVNSVNDLSLEPVGGLYEIQIPSEFTIGNMEEFIQISSPKVTIDCSAFVCGDYAACKSQ	840
Sbjct	781	PFTVN VNDL PVGGLYEIQIPSEFTIGNMEEFIQ SPKVTIDC FVCGDYAACKSQ	840
Query	841	LVEYGSFCDNINAILTEVNELLDTTQLQVANSMLMNGVTLSTKLKDG VNFNVDDINFSPVL	900

Sbjct	841	LVEYGSFCDNINAILTEVNELLDDTTQLQVANSLMNGVTLSTKLKDG NFNVDDINFSPVL LVEYGSFCDNINAILTEVNELLDDTTQLQVANSLMNGVTLSTKLKDG NFNVDDINFSPVL	900
Query	901	GCLGSDCNKVSSRSAIEDLLFSKVKLSDVGFVEAYNNCTGGAEIRDLCVQSYNGIKVLP GCLGS+CNKVSSRSAIEDLLFSKVKLSDVGFV+AYNNCTGGAEIRDLCVQSYNGIKVLP	960
Sbjct	901	GCLGSECNKVSSRSAIEDLLFSKVKLSDVGFVDAYNNCTGGAEIRDLCVQSYNGIKVLP	960
Query	961	PLLSENQISGYTLAATSASLFPPWSAAAGVPFYLNQYRINGIGVTMDVLSQNQKLIANA PLLSENQISGYTLAAT ASLFPPWSAAAGVPFYLNQYRINGIGVTMDVL+QNQKLI+NA	1020
Sbjct	961	PLLSENQISGYTLAATFASLFPPWSAAAGVPFYLNQYRINGIGVTMDVLTQNQKLISNA	1020
Query	1021	FNNALDAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSNRFGAIISSSLQEILSRDA FNNALDAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSN+FGAIS+SLQEILSRDA	1080
Sbjct	1021	FNNALDAIQEGFDATNSALVKIQAVVNANAEALNNLLQQLSNKFGAISASLQEILSRDA	1080
Query	1081	LEAQAQIDRLINGRLTALNAYVSQQLS DSTLVKFSAAQAMEKVNCEVKSQSSRINFCGNG LEAQAQIDRLINGRLTALNAYVSQQLS DSTLVKFSAAQAMEKVNCEVKSQSSRINFCGNG	1140
Sbjct	1081	LEAQAQIDRLINGRLTALNAYVSQQLS DSTLVKFSAAQAMEKVNCEVKSQSSRINFCGNG	1140
Query	1141	NHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFT NHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFT	1200
Sbjct	1141	NHIISLVQNAPYGLYFIHFSYVPTKYVTAKVSPGLCIAGDRGIAPKSGYFVNVNNTWMFT	1200
Query	1201	GSGYYYPEPITGNNVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTSVAPD GSGYYYPEPITGNNVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTSVAPD +APD	1260
Sbjct	1201	GSGYYYPEPITGNNVVMSTCAVNYTKAPDVMLNISTPNLPDFKEELDQWFKNQTLMAPD	1260
Query	1261	LSLDYINVTFLDLQDEMNRLQEAIKVLNQSYINLKDIGTYEYYVKWPWYVWLLIGLAGVA LSLDYINVTFLDLQDEMNRLQEAIKVLN SYINLKDIGTYEYYVKWPWYVWLLIGLAGVA	1320
Sbjct	1261	LSLDYINVTFLDLQDEMNRLQEAIKVLNHSYINLKDIGTYEYYVKWPWYVWLLIGLAGVA	1320
Query	1321	MLVLLFFICCCTGCGTSCFKKCGGCCDDYTGHQELVIKTSRDD 1363 MLVLLFFICCCTGCGTSCFKKCGGCCDDYTGHQELVIKTSRDD	
Sbjct	1321	MLVLLFFICCCTGCGTSCFKKCGGCCDDYTGHQELVIKTSRDD 1363	

CPU time: 0.05 user secs. 0.03 sys. secs 0.08 total secs.